

1  
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51  
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101  
GAAGCAAACC CTTAAGAACG TCACAACTA CTTACTGAT ATCATCTGCA  
151  
AGCGTGCAGA TCTTGGTTAC AACTATGGGG TTATCCTTAT ACCAGAAGGC  
201  
CTGATTGATT TCATCCCAGA GGTTCAAAA CTCATCGCAG AATTGAATGA  
251  
AATTTTGGCA CATGATGTGG TTGATGAGGC AGGGGCCTGG AAAAGCAAGC  
301  
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351  
GAGCAACTTA TGCTTGAAAG GGGCCCCCAT GGCAATGTT AGGTTGCAAA  
401  
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AGAGAAAAGC AGAGGGGAGA TACTCTGCAC ATTTAGAGG GCAAGCTCAT  
501  
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551  
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601  
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751  
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851  
TGACTCGAAC CACACTTTGA TGCTGGAAC CGGTGCTGAG TTATAGAGAT  
901  
GCGTCCTTTG CTTATTTTTG TTTCTTACAG TTTTGGGAGT GGAGACTGGA  
951  
CACTGGGTCT CCTGGAGCAG CCTGCAGTCT CCATATTGTG AATTGTTAA  
1001  
TAAGAGGTTG GATGTGAGTT TTCTGCGTAG CGGACTGGAT GTAGCAAATA  
1051  
AGAACTGGTT TTAGCATTTT TTGTATGATT TACGCACCAA CTGACTTGTC  
1101  
TTGTAACCTT GATTCTGTTT CACTGGTTGC /ATCTCGTGA GAATGAACAA  
1151  
GTTGATATGA GGCTAAATCG GAATTC

Figure 1.

1  
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51  
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151  
ACGGGGAACC CGGATGAGAT CGCGAAGCTG TTCCCTAACT TGTTCGGCA  
201  
GCCGTCGGCG ACATTGGTGC CGGCCAAAGA GCGGTGGAG GGGAAGGCGC  
251  
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301  
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401  
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451  
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501  
GCAAGCCGAA GATACAGCCA ACAAATTGA GTTGGACGGA CTTGTTGTTA  
551  
TTGGACGGGA CGATTCAAAT ACTCATGCTT GCCTCTTTGC TGAATACTC  
601  
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651  
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751  
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851  
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901  
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951  
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1001  
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1051  
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1101  
GTTTTTGCCC AAAACTATTC AGGAGCAACT TATGCTTGAA AGGGGCCCCC  
1151  
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1201  
ATGGTGGAAT CTGAACTGGA GAAGAGAAA GCAGAGGGGA GATACTCTGC

Figure 2

1251  
ACATTTTCAGA GGGCAAGCTC ATTTCTTTGG GTACGAAGGA AGATGTGGCC  
1301  
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1351  
GGTGCCCTTC TCCAAAGTGG GAAGACAGGA CTTATTTTCAT CGGTTGGCAA  
1401  
CCTTGCGGCT CCAGTAGAAG AATGGACTGT TGGTGGAACA GCATTGACAT  
1451  
CACTGATGGA TGTGGAGAGG AGGCATGGCA AGTTCAAGCC AGTGATCGAG  
  
1501  
AAGGCTATGG TGGAACCTGA TGCTGCACCT TTCAAGAAAT ATGCATCAAT  
1551  
GCGGGATGAG TGGGCCACCA AGAACAGATA CATCAGCCCT GGCCCCATCC  
1601  
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Figure 2 cont.

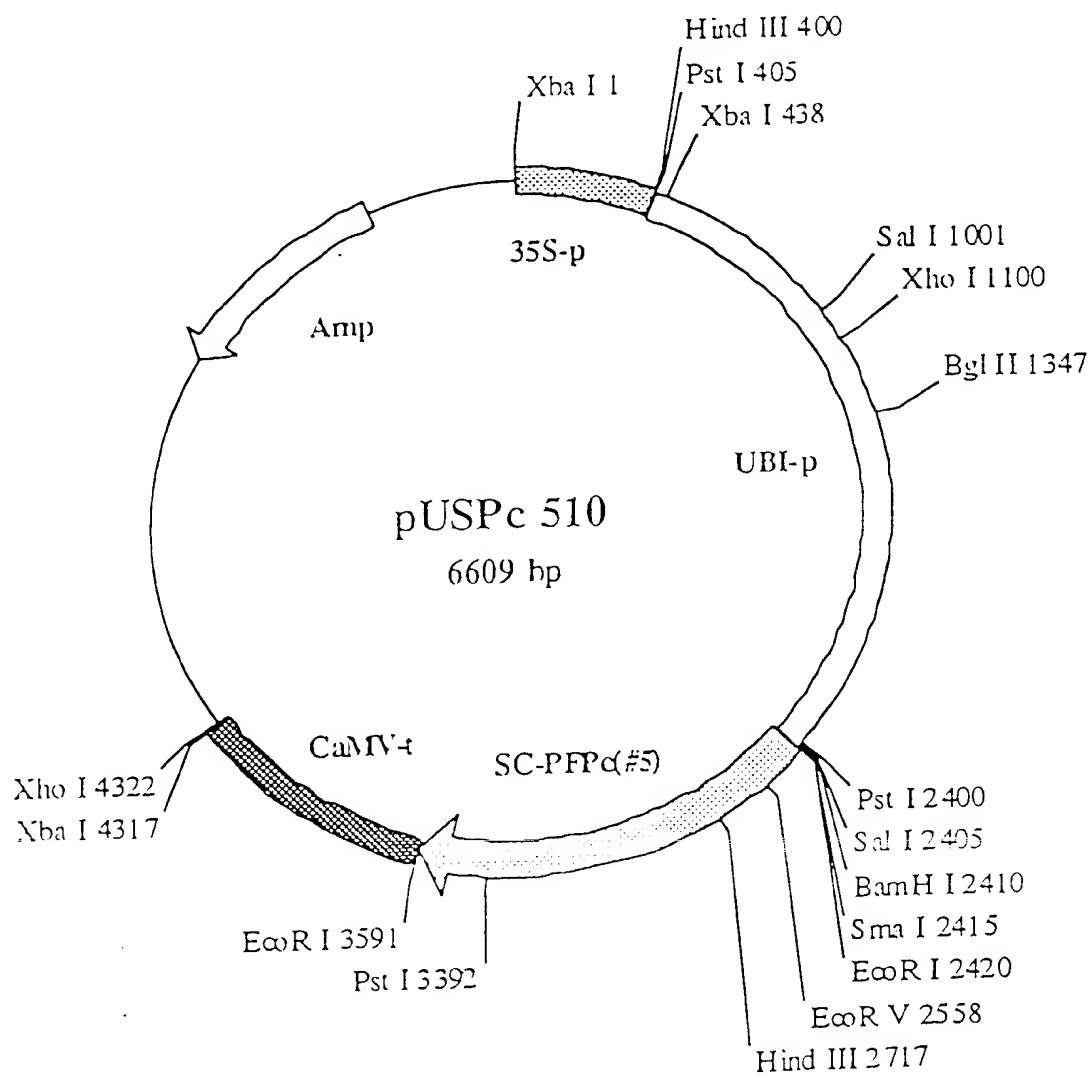


Figure 3

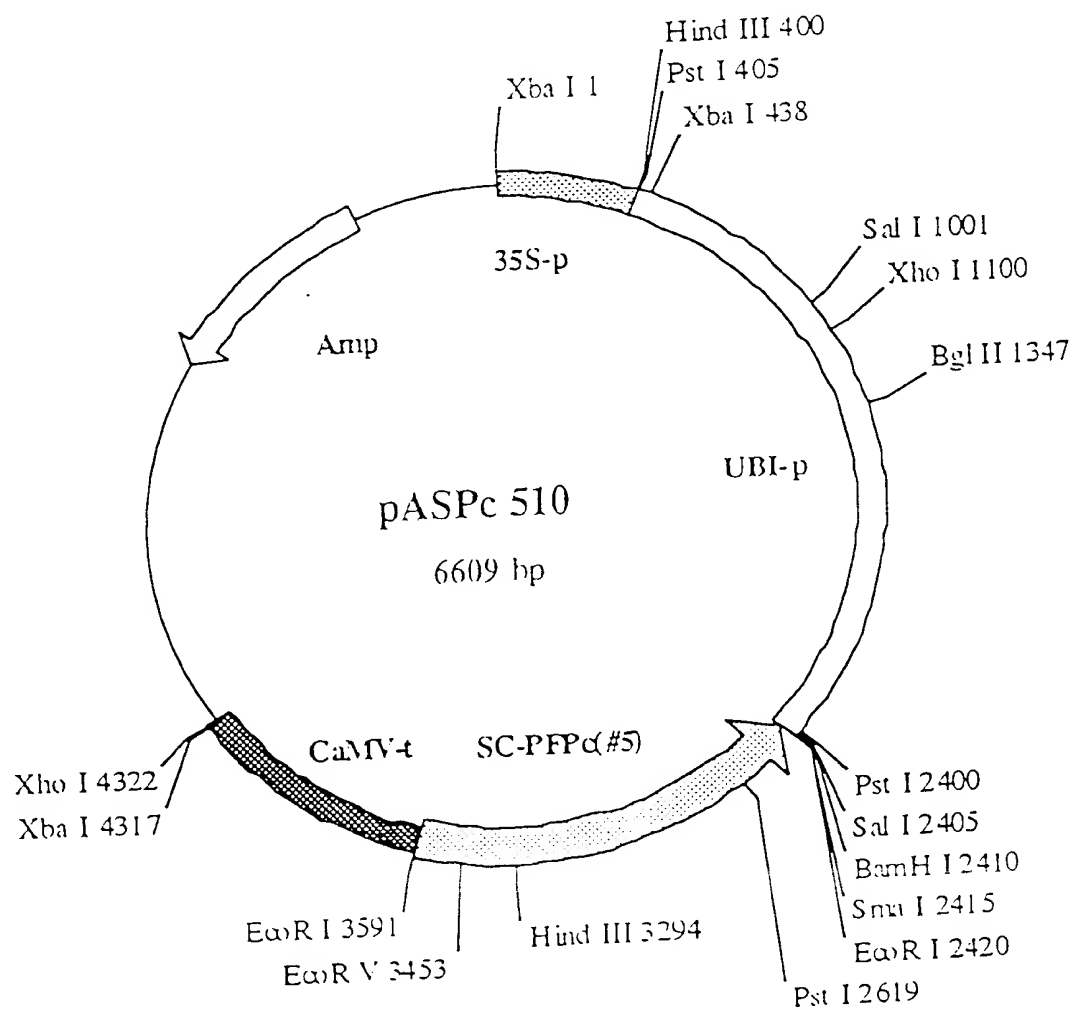


Figure 4

1 2 3 4 5 6 7 8 9 10 11 12

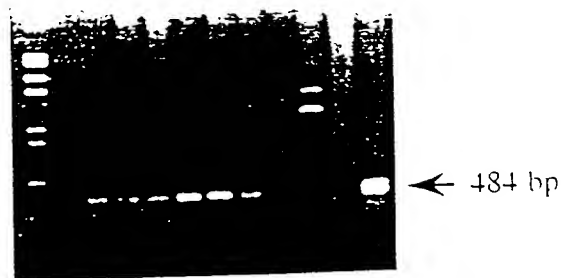


Figure 5.

1 2 3 4 5

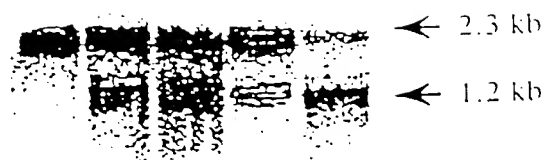


Figure 6

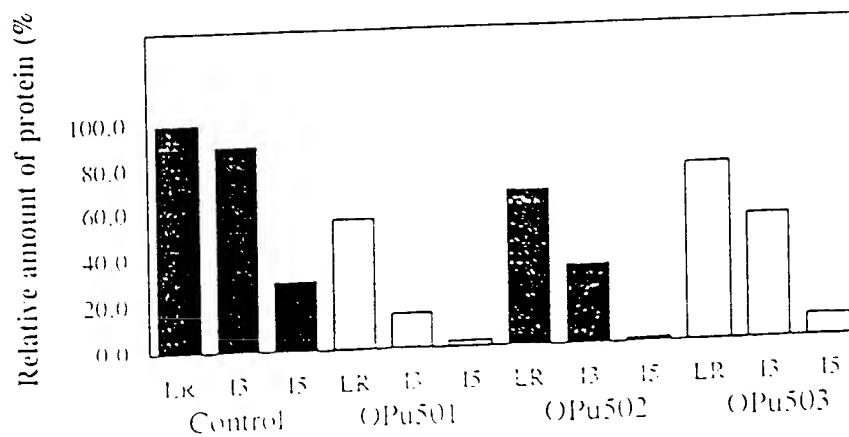


Figure 7